

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 25.6395 Seconds
(without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613b-8

Perfect score: 582

Sequence: 1 MDWLTFQKKHLTFRDVC.....TFVTCENQAPVHFVGVGHC 105

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

3PREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_protist:*
11: sp_rhodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	560	96.2	127	13	Q918V8 rana pipien
2	538	92.4	127	13	Q8UVX5 rana pipien
3	386.5	66.4	129	13	Q9DFY6 rana catesb
4	371	63.7	128	13	Q9DFY8 rana catesb
5	296	50.5	128	13	Q9DFY7 rana catesb
6	294	50.5	128	13	Q9DFY5 rana catesb
7	283	48.6	133	13	Q98SM0 rana catesb
8	277	47.6	133	13	Q9PMK7 rana catesb
9	271	46.6	133	13	Q9SLI9 rana catesb
10	270	46.4	132	13	Q98SM2 rana catesb
11	267	45.9	133	13	Q98SM8 rana catesb
12	265	45.5	132	13	Q98SM1 rana catesb
13	260.5	44.8	132	13	Q9DFY8 rana catesb
14	149.5	25.7	169	13	Q9W738 xenopus lae
15	119	20.4	157	11	Q9JKJ3 meriones un
16	119	20.4	157	11	Q9JKI9 meriones un

17	117	20.1	152	11	Q9JKI5 mus saxicol
18	117	20.1	157	11	Q9JKJ4 meriones un
19	114.5	19.7	153	11	Q9JKI7 mus saxicol
20	114	19.6	157	11	Q9JKJ2 meriones un
21	114	19.6	157	11	Q9JKJ1 meriones un
22	112.5	19.3	132	6	Q9TV24 galago moho
23	111	19.1	154	11	Q9JKI8 mus saxicol
24	108.5	18.6	155	11	Q9JKH9 mus pahari
25	107.5	18.5	119	6	Q9PV32 gorilla gor
26	107.5	18.5	132	6	Q9TV25 eulemur ful
27	107.5	18.5	155	11	Q9JKI3 mus saxicol
28	106.5	18.3	119	6	Q9TS06 cercopithec
29	106.5	18.3	119	6	Q9TV30 saguinus oe
30	105.5	18.1	155	11	Q9JKH8 mus pahari
31	105	18.0	124	6	Q9TSF2 bos taurus
32	105	18.0	136	11	Q9Z3J6 mus musculu
33	104.5	18.0	155	11	Q9JKI6 mus saxicol
34	104	17.9	124	6	Q95NE6 bubalus bub
35	103.5	17.8	155	11	Q9R134 ratus norv
36	103.5	17.8	155	11	Q9JKI4 mus saxicol
37	103.5	17.8	155	11	Q9JKI2 mus saxicol
38	102.5	17.6	170	6	Q9BEC1 onoclea fragilis
39	102	17.5	144	6	Q9BH14 antilocapra
40	102	17.5	156	11	Q9JKH7 mus caroli
41	102	17.5	156	11	Q9JKG6 mus caroli
42	101.5	17.4	155	11	Q9R125 mus musculu
43	101	17.4	156	11	Q9JKG7 mus caroli
44	101	17.4	156	11	Q9VHS0 mus musculu
45	100.5	17.3	119	6	Q9TVJ1 salmifl sci

ALIGNMENTS

RESULT 1

ID	Q918V8	PRELIMINARY:	PRT:	127 AA.
AC	Q918V8:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Onconase variant repURL precursor.			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.			
OX	NCBI_TaxId=8404;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE=20330357; PubMed=10871370;			
RA	Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;			
RT	"A gender-specific mRNA encoding a cytochrome oxidase contains a			
RT	3' UTR of unusual length and structure."			
RL	Nucleic Acids Res. 28:2375-2382(2000).			
DR	EMBL: AF165133; AAF76935.1;			
DR	HSSP: P22069; IONC.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL 1 23 POTENTIAL.			
SQ	SEQUENCE 127 AA; 14491 MW; B851DC5407AB69B CRC64;			

QY	2	ODWLTFQKKHLTFRDVCNNILSTNLFHCKDKNTFTTSRPPVAKICKGIASNVLT 61
DB	24	ODWLTFQKKHLTFRDVCNNILSTNLFHCKDKNTFTTSRPPVAKICKGIASNVLT 83

OY 62 FEFLSDCNVTSRPPCKYKLLKSTTTCVTCENQAPVHFVGHC 105
DB 84 SEFLSDCNVTSRPPCKYKLLKSTTTCVTCENQAPVHFVGHC 127

RESULT 2

ID 08UVX5 PRELIMINARY: PRT: 127 AA.
AC 08UVX5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Oncogene precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_Taxid=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF32139; AAL54383.1;
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA: 14469 MW: 953590351CFFEF3 CRC64;

Query Match
Best Local Similarity 92.4%; Score 538; DB 13; Length 127;
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 QDMLTFOKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPVKAICKGIISKVLT 61
DB 24 QDMLTFOKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPVKAICKGIISKVLT 83

OY 62 FEFLSDCNVTSRPPCKYKLLKSTTTCVTCENQAPVHFVGHC 105
DB 84 SEFLSDCNVTSRPPCKYKLLKSTTTCVTCENQAPVHFVGHC 127

RESULT 3

ID 09DFY6 PRELIMINARY: PRT: 129 AA.
AC 09DFY6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RC Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242555; AAC31441.2;
DR HSP: P22069; IONC.

DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA: 14724 MW: 826A62882B10ABDA CRC64;

Query Match
Best Local Similarity 66.4%; Score 386.5; DB 13; Length 129;
Matches 68; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

OY 2 QDMLTFOKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPVKAICKGIISKVLT 61
DB 24 QDMLTFOKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPVKAICKGIISKVLT 83

OY 62 FEFLSDCNVTSRPPCKYKLLKSTTTCVTCENQAPVHFVGHC 105
DB 84 SEFLSDCNVTSRPPCKYKLLKSTTTCVTCENQAPVHFVGHC 127

RESULT 4

ID 09DFY8 PRELIMINARY: PRT: 128 AA.
AC 09DFY8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RC Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242553; AAC31439.1;
DR HSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA: 14839 MW: 989719CF52053ECC CRC64;

Query Match
Best Local Similarity 63.7%; Score 371; DB 13; Length 128;
Matches 68; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

OY 2 QDMLTFOKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPVKAICKGIISKVLT 61
DB 24 QDMLTFOKKHLNTRVDYDNNILSTNLFHCKDKNTFTYSRPEPVKAICKGIISKVLT 83

OY 62 FEFLSDCNVTSRPPCKYKLLKSTTTCVTCENQAPVHFVGHC 105
DB 84 FEFLSDCNVTSRPPCKYKLLKSTTTCVTCENQAPVHFVGHC 127

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DR Pfam: PF00074: rnaaseA: 1.
DR ProDom: PD000535: RnaaseA: 1.
DR SMART: SM00092: RNase_Pc: 1.
DR PROSITE: PS00127: RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL
FT CHAIN
FT SEQUENCE
SO 1 23 POTENTIAL.
RC-RNASE6_RIBONUCLEASE
AEBBFD67D266C7C2 CRC64;
128 AA: 14628 MW: 877CFC122C3499E02 CRC64;

Query Match
Best Local Similarity 50.5%; Score 294; DB 13; Length 128;
Matches 54; Conservative 14; Mismatches 36; Indels 0; Gaps 0;

OY 2 QDWLTFOKHLITNRDVCNNILSTNLFHCCKNTFTYSRPEPYKAICGIIASKNVLT 61
DB 24 QDWMTFOKHLITDRKVKCDVEMRKALFDCKRTFTIFARPVQALCKNIKDNVLSR 83
OY 62 FEFILSDCNVTSRPCCKYKLRKSTTFCTVCENQAPVHFVGVGHC 105
DB 84 DVFTLPQCNRKKLPCHYRLDGSSTWITCLTCMKELPIHFAGVGKC 127

RESULT 7
O98SMO PRELIMINARY: PRT: 133 AA.
AC O98SMO:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNase A-type, ribonuclease rc208 precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320.
RA Rosenbery H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351209; AAK30255.1;
DR HSRP; P11916; IBC4.
DR InterPro: IPR001427; RnaaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR ProDom: PD000535; RnaaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL
FT SEQUENCE
SO 1 22 POTENTIAL.
RC-POTENTIAL.
AEBBFD67D266C7C2 CRC64;
133 AA: 14628 MW: 877CFC122C3499E02 CRC64;

Query Match
Best Local Similarity 48.6%; Score 283; DB 13; Length 133;
Matches 53; Conservative 16; Mismatches 34; Indels 8; Gaps 3;

OY 2 QDWLTFOKHLITNRDVCNNILSTNLFHCCKNTFTYSRPEPYKAICGIIASKN 57
DB 23 QNMATFOCKHLITNMISSINCNTIMNNIIVGGCKGVNFTLISSATYKALCTGVI-NMN 81
OY 58 VLTTFEFLSDC--NVTSRPCCKYKLRKSTTFCTVCENQAPVHFVGVGHC 105
DB 82 VLSSTRFQNLNCTRTSLTPRCPCYSSPTRENNYICVKGCENQVPHFAGIGFC 132

RESULT 8
O9PMW7 PRELIMINARY: PRT: 133 AA.
AC O9PMW7:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Ribonuclease precursor.

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GN RCR.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=98165825; PubMed=9497370;
 RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
 RT "The Rana catesbeiana rct gene encoding a cytototoxic ribonuclease.
 RT Tissue distribution, cloning, purification, cytotoxicity, and active
 RT residues for RNase activity."
 RL J. Biol. Chem. 273:6395-6401(1998).
 DR EMBL: AF039104; AAD10702.1;
 DR HSSP: P11916; 1BC4
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT CHAIN 1 22 POTENTIAL.
 FT SIGNAL 23 RIBONUCLEASE.
 SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 47.6%; Score 277; DB 13; Length 133;
 Best Local Similarity 47.7%; Pred. No. 3.4e-24;
 Matches 53; Conservative 16; Mismatches 34; Indels 8; Gaps 3;

OY 2 QDMLTFQKHLLTNTRDVCNNILSTNLF---HCKDKNTFYISRPDPYKAICKGIASKN 57
 DB 23 QWMAFFQCKHIIPTINCNITMDNNIYVGGQCKRVNFTIISATYKATCGVI-MKN 81
 OY 58 VLTTFEFLSDC---NWTSPCKYKLLKSTTFECVTCENQAPVHFGVGHG 105
 DB 82 VLSSTKFDLCTRTSITPRCPYSSKRTETNYICVKCENQPVHFGAGIGRC 132

RESULT 9

O98SL9 PRELIMINARY; PRT; 133 AA.
 AC O98SL9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNase A-type ribonuclease rc212 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana."
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351210; AAK30256.1;
 DR HSSP: P11916; 1BC4
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 1 22 RIBONUCLEASE.
 SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 46.6%; Score 271; DB 13; Length 133;
 Best Local Similarity 45.9%; Pred. No. 1.6e-23;
 Matches 51; Conservative 17; Mismatches 35; Indels 8; Gaps 3;

OY 2 QDMLTFQKHLLTNTRDVCNNILSTNLF---HCKDKNTFYISRPDPYKAICKGIASKN 57
 DB 23 QWMAFFQCKHIIPTINCNITMDNNIYVGGQCKRVNFTIISATYKATCGVI-MKN 81
 OY 58 VLTTFEFLSDC---NWTSPCKYKLLKSTTFECVTCENQAPVHFGVGHG 105
 DB 82 VLSSTKFDLCTRTSITPRCPYSSKRTETNYICVKCENQPVHFGAGIGRC 132

RESULT 10

O98SM2 PRELIMINARY; PRT; 132 AA.
 AC O98SM2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana."
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351207; AAK30253.1;
 DR HSSP: P11916; 1BC4
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 1 22 RC-RNASE7.
 SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 46.4%; Score 270; DB 13; Length 132;
 Best Local Similarity 45.9%; Pred. No. 2.1e-23;
 Matches 51; Conservative 14; Mismatches 38; Indels 8; Gaps 3;

OY 2 QDMLTFQKHLLTNTRDVCNNILSTNLF---HCKDKNTFYISRPDPYKAICKGIASKN 57
 DB 23 QWMAFFQCKHIIPTINCNITMDNNIYVGGQCKRVNFTIISATYKATCGVI-MKN 81
 OY 58 VLTTFEFLSDC---NWTSPCKYKLLKSTTFECVTCENQAPVHFGVGHG 105
 DB 82 VLSSTKFDLCTRTSITPRCPYSSKRTETNYICVKCENQPVHFGAGIGRC 132

RESULT 11

O98SL8 PRELIMINARY; PRT; 133 AA.
 AC O98SL8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNase A-type ribonuclease rc218 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN (1)
 RP SEQUENCE FROM N.A.

RESULT 13

RESULT 14

RP SEQUENCE FROM N.A.
BA Kioshita N Kirschner M W.

